Claims 1-24 (cancelled)

25. (currently amended) A method for identifying compounds that bind to a target of interest, comprising:

selecting a member of a first set of ligands which non-covalently binds to a first binding site of a target biomolecule selected from a polypeptide and a protein, by detecting the non-covalent binding of the member of the first set of ligands to the target biomolecule by mass spectrometry;

selecting a member of a second set of ligands which non-covalently binds to a second binding site of the target biomolecule, by detecting the non-covalent binding of the member of the second set of ligands to the target biomolecule by mass spectrometry;

forming a linked ligand compound by chemically linking the member of the first set of ligands to the member of the second set of ligands;

contacting the linked ligand compound with the target; and

identifying a 1:1 complex of linked ligand compound and target biomolecule by detecting the non-covalent binding of the linked ligand compound to the target biomolecule by mass spectrometry,

wherein the member of the first set of ligands and the member of the second set of ligands each and independently have one or more functional groups selected from hydrogen bond donors, hydrogen bond acceptors, functional groups which form a cation at physiological pH, functional groups which form an anion at physiological pH, and functional groups which form hydrophobic interactions; and wherein the member of the first set of ligands and the member of the second set of ligands do not have all the same functional groups;

wherein the linked ligand compound binds to the target biomolecule with higher affinity than the member of the first set of ligands or the member of the second set of ligands;

whereby the compound that binds to the target is identified.

~~wherein the target biomolecule is selected from a polypeptide, protein, DNA, RNA or polysaccharide.~~

26. (cancelled)

27. (previously presented) The method of claim 25 wherein the member of the first set of ligands and the member of the second set of ligands each have a dissociation constant, K_d, equal to 500 μM or less.

28. (previously presented) The method of claim 27 wherein the dissociation constant of the compound binding to the target is less than the dissociation constant of the member of the first set of ligands or the dissociation constant of the member of the second set of ligands binding to target.

29. (previously presented) The method of claim 25, wherein the first binding site is the same as the second binding site.

30. (previously presented) The method of claim 25, wherein the first binding site is not the same as the second binding site.

31. (previously presented) The method of claim 25 where the protein is selected from cell surface receptor proteins, soluble receptor proteins, proteases, matrix metalloproteinases, clotting factors, serine/threonine kinases, dephosphorylases, tyrosine kinases, bacterial enzymes, fungal enzymes, viral enzymes, signal transduction proteins, transcription factors, proteins associated with DNA and/or RNA synthesis or degradation, immunoglobulins, hormones, and cytokine receptors.

32. (previously presented) The method of claim 31 where the cytokine receptor is selected from erythropoietin/EPO, granulocyte colony stimulating receptor, granulocyte macrophage colony stimulating receptor, thrombopoietin (TPO), IL- 1, IL-2, IL-3, IL-4, IL-5, IL-6, IL- 10, IL- 11, IL- 12, growth hormone, prolactin, human placental lactogen (LPL), CNTF, octostatin, RANTES, MIPI, IL-8, insulin, insulin-like growth factor I (IGF-1), epidermal growth factor (EGF), heregulin-a and heregulin-b, vascular endothelial growth factor (VEGF)1, 2, and 3, placental growth factor (PLGF), tissue growth factor (TGF-(X and TGF-P), bone morphogenic factor, folical stimulating hormone (FSH), luteinizing hormone (LH), tissue necrosis factor (TNF), and apoptosis factor.

33. (previously presented) The method of claim 31 where the dephosphorylase is protein tyrosine phosphatase 1*b* (PTP1*b*).

34. (previously presented) The method of claim 31 where the matrix metalloproteinase is stromelysin.